In the Claims

We claim:

Claims 1-48 (Cancelled)

Claim 49 (New): A composition of matter comprising:

a) an isolated polypeptide selected from the group consisting of:

1) an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

2) a fragment of said amino acid sequence which functions as a biologically active polypeptide and/or has an antigenic determinant in common with a polypeptide according to 1);

3) a functional equivalent of 1) or 2);

4) the functional equivalent of 3), wherein the functional equivalent is homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, and is a C1q and/or collagen domain containing polypeptide;

5) the functional equivalent of 3), wherein the functional equivalent has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

6) the functional equivalent of 3), wherein the functional equivalent has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

7) the functional equivalent of 3), wherein the functional equivalent exhibits significant structural homology with a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

8) the fragment of 2), wherein the fragment has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

9) the fragment of 2), wherein the fragment has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

10) the fragment of 2), wherein the fragment has an antigenic determinant in common with the polypeptide of 1), and wherein the fragment consists of 7 or more amino acid residues from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

11) a fusion protein comprising any of a1) to a10);

12) the fusion protein of 11), further comprising a histidine tag;

13) the fusion protein of 12), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20;

14) the polypeptide of any one of 1) to 13), further comprising a signal peptide; and

15) the polypeptide of 14), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:22 and SEQ ID NO:24;

or

b) a purified nucleic acid molecule:

1) comprising a nucleic acid sequence encoding a polypeptide of any one of a1) to a15); or

2) comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

3) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

4) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23, or is a redundant equivalent or fragment of any of the foregoing; or

5) that hybridizes under high stringency conditions with a nucleic acid molecule of any of b1) to b4); or

c) a vector comprising a nucleic acid molecule according to any one of b1) to b5); or

d) a host cell transformed with a vector or a nucleic acid molecule according to any one of b) or c); or

e) a ligand:

1) that binds specifically to the polypeptide of any of a1) to a15); or

2) which is an antibody that binds specifically to the polypeptide of any of a1) to a15); or

f) a compound:

1) that increases the level of expression or activity of a polypeptide according to any of a1) to a15); or

2) that decreases the level of expression or activity of a polypeptide according to any of a1) to a15); or

g) a compound that binds to a polypeptide according to any of a1) to a15) without inducing any of the biological effects of the polypeptide; or

h) a compound that binds to a polypeptide according to any of a1) to a15) without inducing any of the biological effects of the polypeptide, wherein the compound is a natural or modified substrate, ligand, enzyme, receptor or structural or functional mimetic; or

i) a pharmaceutical composition comprising any one of a) to h), and a pharmaceutically acceptable carrier; or

j) a vaccine composition comprising any one of a1) to a15) or b1) to b5); or

k) a kit for diagnosing disease, comprising a first container containing a nucleic acid probe that hybridizes under stringent conditions with a nucleic acid molecule of any one of b1) to b5), a second container containing primers useful for amplifying the nucleic acid molecule, and instructions for using the probe and primers for facilitating the diagnosis of disease; or

l) a kit for diagnosing disease, comprising a first container containing a nucleic acid probe that hybridizes under stringent conditions with a nucleic acid molecule of any one of b1) to b5); a second container containing primers useful for amplifying the nucleic acid molecule; a third container holding an agent for digesting unhybridized RNA; and instructions for using the probe and primers for facilitating the diagnosis of disease; or

m) a kit comprising an array of nucleic acid molecules, at least one of which is a nucleic acid molecule according to any one of b1) to b5); or

n) a kit comprising one or more antibodies that bind to a polypeptide as recited in any one of a1) to a15); and a reagent useful for the detection of a binding reaction between the one or more antibodies and the polypeptide; or

o) a transgenic or knockout non-human animal that has been transformed to express higher, lower, or absent levels of a polypeptide according to any one of a1) to a15).

Claim 50 (New): A method of using a composition of matter, comprising obtaining a composition of matter according to claim 49 and using said composition of matter in a method selected from the group consisting of: diagnosing a disease in a patient; treatment of a disease in a patient; monitoring the therapeutic treatment of a disease; identification of a compound that is effective in the treatment and/or diagnosis of a disease; and screening candidate compounds.

Claim 51 (New): The method of claim 50, wherein said method of using a composition of matter comprises the method for treatment of a disease, comprising administering to the patient:

a) an isolated polypeptide selected from the group consisting of:

1) an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

2) a fragment of said amino acid sequence which functions as a biologically active polypeptide and/or has an antigenic determinant in common with a polypeptide according to 1);

3) a functional equivalent of 1) or 2);

4) the functional equivalent of 3), wherein the functional equivalent is homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, and is a C1q and/or collagen domain containing polypeptide;

5) the functional equivalent of 3), wherein the functional equivalent has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

6) the functional equivalent of 3), wherein the functional equivalent has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of

SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

7) the functional equivalent of 3), wherein the functional equivalent exhibits significant structural homology with a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

8) the fragment of 2), wherein the fragment has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

9) the fragment of 2), wherein the fragment has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

10) the fragment of 2), wherein the fragment has an antigenic determinant in common with the polypeptide of 1), and wherein the fragment consists of 7 or more amino acid residues from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

11) a fusion protein comprising any of a1) to a10);

12) the fusion protein of 11), further comprising a histidine tag;

13) the fusion protein of 12), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20;

14) the polypeptide of any one of 1) to 13), further comprising a signal peptide; and

15) the polypeptide of 14), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:22 and SEQ ID NO:24; or

b) a purified nucleic acid molecule:

1) comprising a nucleic acid sequence encoding a polypeptide of any one of a1) to a15); or

2) comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

3) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

4) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23, or is a redundant equivalent or fragment of any of the foregoing; or

5) that hybridizes under high stringency conditions with a nucleic acid molecule of any of b1) to b4); or

c) a vector comprising a nucleic acid molecule according to any one of b1) to b5); or

d) a host cell transformed with a vector or a nucleic acid molecule according to any one of b) or c); or

e) a ligand:

1) that binds specifically to the polypeptide of any of a1) to a15); or

2) which is an antibody that binds specifically to the polypeptide of any of a1) to a15); or

f) a compound:

1) that increases the level of expression or activity of a polypeptide according to any of a1) to a15); or

2) that decreases the level of expression or activity of a polypeptide according to any of a1) to a15); or

g) a compound that binds to a polypeptide according to any of a1) to a15) without inducing any of the biological effects of the polypeptide; or

h) a compound that binds to a polypeptide according to any of a1) to a15) without inducing any of the biological effects of the polypeptide, wherein the compound is a natural or modified substrate, ligand, enzyme, receptor or structural or functional mimetic; or

i) a pharmaceutical composition comprising any one of a) to h), and a pharmaceutically acceptable carrier.

Claim 52 (New): The method of claim 51, wherein the disease includes one or more of among an autoimmune disease, autoimmune inner ear disease, Labyrinthitis, Ménière disease and Ménière syndrome, Perilymphatic or labyrinthine fistula, Tinnitus, neurodegenerative disease,

amyloidosis, Alzheimer's disease, Parkinson's disease, familial dementia, inflammation, microbial infection, bacterial infection, viral infection (HIV, HTLV or MuLV infections), parasitic infection, SLE, glomerulonephritis, obesity, diabetes, Schmid metaphyseal chondrodysplasia, corneal endothelial dystrophy, posterior polymorphous corneal dystrophy (PPCD), Fuchs endothelial corneal dystrophy (FECD), atherosclerosis, scurvy, cancer, gastrointestinal stromal tumors, osteosarcoma, chondroblastoma, giant cell tumor, spondylometaphyseal dysplasia Japanese type (SMD), Osteogenesis Imperfecta, Ehlers-Danlos syndrome, susceptibility to dissection of cervical arteries, Ehlers-Danlos syndrome, aortic aneurysm, otospondylomegaepiphyseal dysplasia, hearing loss (deafness), Weissenbacher-Zweymuller syndrome, arthritis, bone or skeletal disease, late-onset retinal degeneration (L-ORD), age-related macular degeneration (AMD) and/or blindness.

Claim 53 (New): The method of claim 51, wherein the disease is one for which the expression of the natural gene or the activity of the polypeptide is lower in a diseased patient when compared to the level of expression or activity in a healthy patient, the polypeptide, nucleic acid molecule, vector, ligand, compound or composition administered to the patient is an agonist.

Claim 54 (New): The method of claim 51, wherein the disease is one for which expression of the natural gene or activity of the polypeptide is higher in a diseased patient when compared to the level of expression or activity in a healthy patient, the polypeptide, nucleic acid molecule, vector, ligand, compound or composition administered to the patient is an antagonist.

Claim 55 (New): The method of claim 50, wherein said method of using a composition of matter comprises the method for diagnosing a disease in a patient, comprising assessing the level of expression of a natural gene encoding a polypeptide, or assessing the activity of the polypeptide, in tissue from said patient; and comparing said level of expression or activity to a control level, wherein a level that is different to said control level is indicative of disease, and wherein the polypeptide:

a) comprises an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10; or

b) comprises a fragment of said amino acid sequence which functions as a biologically active polypeptide and/or has an antigenic determinant in common with a polypeptide according to a); or

c) a functional equivalent of a) or b); or

d) the functional equivalent of d), wherein the functional equivalent is homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, and is a C1q and/or collagen domain containing polypeptide; or

e) the functional equivalent of c), wherein the functional equivalent has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

f) the functional equivalent of c), wherein the functional equivalent has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

g) the functional equivalent of c), wherein the functional equivalent exhibits significant structural homology with a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10; or

h) the fragment of b), wherein the fragment has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

i) the fragment of b), wherein the fragment has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

j) the fragment of b), wherein the fragment has an antigenic determinant in common with the polypeptide of a), and wherein the fragment consists of 7 or more amino acid residues from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10; or

k) a fusion protein comprising any of a) to j); or

l) the fusion protein of k), further comprising a histidine tag; or

m) the fusion protein of l), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20; or

n) the polypeptide of any one of a) to m), further comprising a signal peptide; or

o) the polypeptide of n), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:22 and SEQ ID NO:24.

Claim 56 (New): The method of claim 55, which is carried out *in vitro*.

Claim 57 (New): The method of claim 55, comprising:

a) contacting a ligand with a biological sample under conditions suitable for the formation of a ligand-polypeptide complex; and

b) detecting said complex, wherein the ligand binds specifically to the polypeptide of any of a) to o) of claim 55, or wherein the ligand is an antibody that binds specifically to the polypeptide of any of a) to o) of claim 55.

Claim 58 (New): The method of claim 55, comprising:

a) contacting a sample of tissue from the patient with a nucleic acid probe under stringent conditions that allow the formation of a hybrid complex between a nucleic acid molecule and the probe;

b) contacting a control sample with said probe under the same conditions used in step a); and

c) detecting the presence of hybrid complexes in said samples; wherein detection of levels of the hybrid complex in the patient sample that differ from levels of the hybrid complex in the control sample is indicative of disease, wherein the nucleic acid molecule:

1) comprises a nucleic acid sequence encoding a polypeptide according to any one of a) – o) of claim 55; or

2) comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

3) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

4) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23, or is a redundant equivalent or fragment of any of the foregoing; or

5) hybridizes under high stringency conditions with a nucleic acid molecule of any of c1) to c4).

Claim 59 (New): The method of claim 55, comprising:

a) contacting a sample of nucleic acid from tissue of the patient with a nucleic acid primer under stringent conditions that allow the formation of a hybrid complex between a nucleic acid molecule and the primer;

b) contacting a control sample with said primer under the same conditions used in step a);

c) amplifying the sampled nucleic acid; and

d) detecting the level of amplified nucleic acid from both patient and control samples; wherein detection of levels of the amplified nucleic acid in the patient sample that differ significantly from levels of the amplified nucleic acid in the control sample is indicative of disease, wherein the nucleic acid molecule:

1) comprises a nucleic acid sequence encoding a polypeptide according to any one of a) – o) of claim 55; or

2) comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

3) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

4) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23, or is a redundant equivalent or fragment of any of the foregoing; or

5) hybridizes under high stringency conditions with a nucleic acid molecule of any of d1) to d4).

Claim 60 (New): The method of claim 55, comprising:

a) obtaining a tissue sample from a patient being tested for disease;

b) isolating a nucleic acid molecule from said tissue sample; and

c) diagnosing the patient for disease by detecting the presence of a mutation which is associated with disease in the nucleic acid molecule as an indication of the disease, wherein the nucleic acid molecule:

1) comprises a nucleic acid sequence encoding a polypeptide according to any one of a) – o) of claim 55; or

2) comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

3) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

4) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23, or is a redundant equivalent or fragment of any of the foregoing; or

5) hybridizes under high stringency conditions with a nucleic acid molecule of any of c1) to c4).

Claim 61 (New): The method of claim 60, further comprising amplifying the nucleic acid molecule to form an amplified product and detecting the presence or absence of a mutation in the amplified product.

Claim 62 (New): The method of claim 60, wherein the presence or absence of the mutation in the patient is detected by contacting said nucleic acid molecule with a nucleic acid probe that hybridizes to said nucleic acid molecule under stringent conditions to form a hybrid double-stranded molecule, the hybrid double-stranded molecule having an unhybridized portion

of the nucleic acid probe strand at any portion corresponding to a mutation associated with disease; and detecting the presence or absence of an unhybridized portion of the probe strand as an indication of the presence or absence of a disease-associated mutation.

Claim 63 (New): The method of claim 55, wherein said disease includes one or more of among an autoimmune disease, autoimmune inner ear disease, Labyrinthitis, Ménière disease and Ménière syndrome, Perilymphatic or labyrinthine fistula, Tinnitus, neurodegenerative disease, amyloidosis, Alzheimer's disease, Parkinson's disease, familial dementia, inflammation, microbial infection, bacterial infection, viral infection (HIV, HTLV or MuLV infections), parasitic infection, SLE, glomerulonephritis, obesity, diabetes, Schmid metaphyseal chondrodysplasia, corneal endothelial dystrophy, posterior polymorphous corneal dystrophy (PPCD), Fuchs endothelial corneal dystrophy (FECD), atherosclerosis, scurvy, cancer, gastrointestinal stromal tumors, osteosarcoma, chondroblastoma, giant cell tumor, spondylometaphyseal dysplasia Japanese type (SMD), Osteogenesis Imperfecta, Ehlers-Danlos syndrome, susceptibility to dissection of cervical arteries, Ehlers-Danlos syndrome, aortic aneurysm, otospondylomegaepiphyseal dysplasia, hearing loss (deafness), Weissenbacher-Zweymuller syndrome, arthritis, bone or skeletal disease, late-onset retinal degeneration (L-ORD), age-related macular degeneration (AMD) and/or blindness.

Claim 64 (New): The method of claim 50, wherein said method of using a composition of matter comprises the method of monitoring the therapeutic treatment of a disease, comprising monitoring over a period of time the level of expression or activity of a polypeptide, or the level of expression of a nucleic acid molecule, in tissue from said patient, wherein altering said level of expression or activity over the period of time towards a control level is indicative of regression of said disease, wherein

a) the polypeptide is selected from the group consisting of:

1) an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

2) a fragment of said amino acid sequence which functions as a biologically active polypeptide and/or has an antigenic determinant in common with a polypeptide according to 1);

3) a functional equivalent of 1) or 2);

4) the functional equivalent of 3), wherein the functional equivalent is homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, and is a C1q and/or collagen domain containing polypeptide;

5) the functional equivalent of 3), wherein the functional equivalent has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

6) the functional equivalent of 3), wherein the functional equivalent has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

7) the functional equivalent of 3), wherein the functional equivalent exhibits significant structural homology with a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

8) the fragment of 2), wherein the fragment has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

9) the fragment of 2), wherein the fragment has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

10) the fragment of 2), wherein the fragment has an antigenic determinant in common with the polypeptide of 1), and wherein the fragment consists of 7 or more amino acid residues from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

11) a fusion protein comprising any of a1) to a10);

12) the fusion protein of 11), further comprising a histidine tag;

13) the fusion protein of 12), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20;

14) the polypeptide of any one of 1) to 13), further comprising a signal peptide; and

15) the polypeptide of 14), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:22 and SEQ ID NO:24; and wherein

b) the nucleic acid molecule:

1) encodes a polypeptide of any one of a1) to a15); or

2) comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

3) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

4) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23, or is a redundant equivalent or fragment of any of the foregoing; or

5) that hybridizes under high stringency conditions with a nucleic acid molecule of any of b1) to b4).

Claim 65 (New): The method of claim 64, wherein the disease includes one or more of among an autoimmune disease, autoimmune inner ear disease, Labyrinthitis, Ménière disease and Ménière syndrome, Perilymphatic or labyrinthine fistula, Tinnitus, neurodegenerative disease, amyloidosis, Alzheimer's disease, Parkinson's disease, familial dementia, inflammation, microbial infection, bacterial infection, viral infection (HIV, HTLV or MuLV infections), parasitic infection, SLE, glomerulonephritis, obesity, diabetes, Schmid metaphyseal chondrodysplasia, corneal endothelial dystrophy, posterior polymorphous corneal dystrophy (PPCD), Fuchs endothelial corneal dystrophy (FECD), atherosclerosis, scurvy, cancer, gastrointestinal stromal tumors, osteosarcoma, chondroblastoma, giant cell tumor, spondylometaphyseal dysplasia Japanese type (SMD), Osteogenesis Imperfecta, Ehlers-Danlos syndrome, susceptibility to dissection of cervical arteries, Ehlers-Danlos syndrome, aortic aneurysm, otospondylomegaepiphyseal dysplasia, hearing loss (deafness), Weissenbacher-

Zweymuller syndrome, arthritis, bone or skeletal disease, late-onset retinal degeneration (L-ORD), age-related macular degeneration (AMD) and/or blindness.

Claim 66 (New): The method of claim 50, wherein said method of using a composition of matter comprises the method for identification of a compound that is effective in the treatment and/or diagnosis of a disease, comprising contacting a polypeptide or a nucleic acid molecule of with one or more compounds suspected of possessing binding affinity for said polypeptide or nucleic acid molecule, and selecting a compound that binds specifically to said nucleic acid molecule or polypeptide, wherein

a) the polypeptide is selected from the group consisting of:

1) an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

2) a fragment of said amino acid sequence which functions as a biologically active polypeptide and/or has an antigenic determinant in common with a polypeptide according to 1);

3) a functional equivalent of 1) or 2);

4) the functional equivalent of 3), wherein the functional equivalent is homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, and is a C1q and/or collagen domain containing polypeptide;

5) the functional equivalent of 3), wherein the functional equivalent has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

6) the functional equivalent of 3), wherein the functional equivalent has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

7) the functional equivalent of 3), wherein the functional equivalent exhibits significant structural homology with a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

8) the fragment of 2), wherein the fragment has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

9) the fragment of 2), wherein the fragment has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof;

10) the fragment of 2), wherein the fragment has an antigenic determinant in common with the polypeptide of 1), and wherein the fragment consists of 7 or more amino acid residues from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10;

11) a fusion protein comprising any of a1) to a10);

12) the fusion protein of 11), further comprising a histidine tag;

13) the fusion protein of 12), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20;

14) the polypeptide of any one of 1) to 13), further comprising a signal peptide; and

15) the polypeptide of 14), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:22 and SEQ ID NO:24; and wherein

b) the nucleic acid molecule:

1) encodes a polypeptide of any one of a1) to a15); or

2) comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

3) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23; or

4) consists of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:23, or is a redundant equivalent or fragment of any of the foregoing; or

5) that hybridizes under high stringency conditions with a nucleic acid molecule of any of b1) to b4).

Claim 67 (New): The method of claim 66, wherein the disease includes one or more of among an autoimmune disease, autoimmune inner ear disease, Labyrinthitis, Ménière disease and Ménière syndrome, Perilymphatic or labyrinthine fistula, Tinnitus, neurodegenerative disease, amyloidosis, Alzheimer's disease, Parkinson's disease, familial dementia, inflammation, microbial infection, bacterial infection, viral infection (HIV, HTLV or MuLV infections), parasitic infection, SLE, glomerulonephritis, obesity, diabetes, Schmid metaphyseal chondrodysplasia, corneal endothelial dystrophy, posterior polymorphous corneal dystrophy (PPCD), Fuchs endothelial corneal dystrophy (FECD), atherosclerosis, scurvy, cancer, gastrointestinal stromal tumors, osteosarcoma, chondroblastoma, giant cell tumor, spondylometaphyseal dysplasia Japanese type (SMD), Osteogenesis Imperfecta, Ehlers-Danlos syndrome, susceptibility to dissection of cervical arteries, Ehlers-Danlos syndrome, aortic aneurysm, otospondylomegaepiphyseal dysplasia, hearing loss (deafness), Weissenbacher-Zweymuller syndrome, arthritis, bone or skeletal disease, late-onset retinal degeneration (L-ORD), age-related macular degeneration (AMD) and/or blindness.

Claim 68 (New): The method of claim 50, wherein said method of using a composition of matter comprises the method for screening candidate compounds, comprising contacting a non-human transgenic animal with a candidate compound and determining the effect of the compound on the disease of the transgenic animal, wherein the transgenic animal has been transformed to express higher, lower, or absent levels of a polypeptide, wherein the polypeptide:

a) comprises an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10; or

b) comprises a fragment of said amino acid sequence which functions as a biologically active polypeptide and/or has an antigenic determinant in common with a polypeptide according to a); or

c) a functional equivalent of a) or b); or

d) the functional equivalent of d), wherein the functional equivalent is homologous to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ

ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, and is a C1q and/or collagen domain containing polypeptide; or

e) the functional equivalent of c), wherein the functional equivalent has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

f) the functional equivalent of c), wherein the functional equivalent has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

g) the functional equivalent of c), wherein the functional equivalent exhibits significant structural homology with a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10; or

h) the fragment of b), wherein the fragment has greater than 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

i) the fragment of b), wherein the fragment has greater than 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10, or with an active fragment thereof; or

j) the fragment of b), wherein the fragment has an antigenic determinant in common with the polypeptide of a), and wherein the fragment consists of 7 or more amino acid residues from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10; or

k) a fusion protein comprising any of a) to j); or

l) the fusion protein of k), further comprising a histidine tag; or

m) the fusion protein of l), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20; or

n) the polypeptide of any one of a) to m), further comprising a signal peptide; or

o) the polypeptide of n), comprising an amino acid sequence selected from the group consisting of SEQ ID NO:22 and SEQ ID NO:24.

Claim 69 (New): The method of claim 68, wherein the disease includes one or more of among an autoimmune disease, autoimmune inner ear disease, Labyrinthitis, Ménière disease and Ménière syndrome, Perilymphatic or labyrinthine fistula, Tinnitus, neurodegenerative disease, amyloidosis, Alzheimer's disease, Parkinson's disease, familial dementia, inflammation, microbial infection, bacterial infection, viral infection (HIV, HTLV or MuLV infections), parasitic infection, SLE, glomerulonephritis, obesity, diabetes, Schmid metaphyseal chondrodysplasia, corneal endothelial dystrophy, posterior polymorphous corneal dystrophy (PPCD), Fuchs endothelial corneal dystrophy (FECD), atherosclerosis, scurvy, cancer, gastrointestinal stromal tumors, osteosarcoma, chondroblastoma, giant cell tumor, spondylometaphyseal dysplasia Japanese type (SMD), Osteogenesis Imperfecta, Ehlers-Danlos syndrome, susceptibility to dissection of cervical arteries, Ehlers-Danlos syndrome, aortic aneurysm, otospondylomegaepiphyseal dysplasia, hearing loss (deafness), Weissenbacher-Zweymuller syndrome, arthritis, bone or skeletal disease, late-onset retinal degeneration (L-ORD), age-related macular degeneration (AMD) and/or blindness.

Claim 70 (New): An isolated polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, and SEQ ID NO:10.

Claim 71 (New): An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, and SEQ ID NO:24.